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GAT GAC GTC AAA AAC GGA GTT AAA GGA AAT GGA GTT CCA AAA GTG TTA AAA CAA AAA GGA D D V K N G V K G N G V P K V L K Q K G 301

GGC ACT GCT TGG GTT GAT GGA GAA AAT CTT CTG GGT GCA GTT GTT GGA AAC TTC TGT ACC G T A W V D G E N L L G A V V G N F C T

GAC TTG GCT ATT AAA TTG GCT AAA GAA TTT GGC GTT GCT TGG GTG GTA ACA AAA AAT TCT D L A I K L A K E F G V A W V V T K N S

AAT CAT TAT GGA GCT TGT CAA CAT TAT ACT AAG AAA ATT GCA AAT GCA GGA ATG GTG GGA N H Y G A C Q H Y T K K I A N A G M V G 481

ATG TCT TTT ACA AAT ACA TCG CCT CTC ATG TTC CCC TGC CGA TCT TCT GAG ATT GGA CTT M S F T N T S P L M F P C R S S E I G L

GAC ATG GCT ACG ACA ACT GTT GCT CTT GGA AAG GTA GAG CTG GCA GAT TGT CGC GGT AAA

D M A T T T V A L G K V E L A D C R G K

661

ACA CAA ATT CCC TCC ACA TGG GGT GCC GAT TCT AAA GGC AAT CCA TCG ACT GAT ACA CAA T Q I P S T W G A D S K G N P S T D T Q 721

GTT GTT TTA CAC GGT GGC GGA CTT TTG CCT TTA GGC GGT ATA GAA GAG ACG GGA TCT TAC V V L H G G G L L P L G G I E E T G S Y

AAA GGA ACG GGT CTT TCA ATG ATG GGT GAA TTG TTT TGT GGA ATT TTG GCA GGG TCA AGT K G T G L S M M G E L F C G I L A G S S 841

781

TTT GGA AAA AAT GTA CGA TTA TGG GGG CAA TCA CAC AAA GCC GCT GAC AAT GGC CAA TGT F G K N V R L W G Q S H K A A D N G Q C

TTT GTT GCT ATT GAT CAA GAA TGT TTT GCC CCA GGA TTT GCT CCT CGT TTA CAA CAA TTT F V A I D Q E C F A P G F A P R L Q Q F 961

TTG GAT GAA ACA CGG AAT TTG AAA CCG ATT TCT GAA GAA AAG CCT GTT CTA GTG CCT GGA L D E T R N L K P I S E E K P V L V P G 1021

GAT CCT GAA AGA ATG AAT ACA GAA TAT AGC CAA AAG GCT GGA GGT TTG GTA TAC CAA GAA D P E R M N T E Y S Q K A G G L V Y Q E 1081

GGG CAG ATA AAA GCT TTG GAA GAG TTG GCC ACA AAA TGT GAT GTT CAA ATG TTC TCA TAC G Q I K A L E E L A T K C D V Q M F S Y 1141

AAA CGA CTA AAA tga gga tga gat tta aat att ttt ttg tgt agc tga aac tga ctt caa K R L K  $\star^{\circ}$  1201

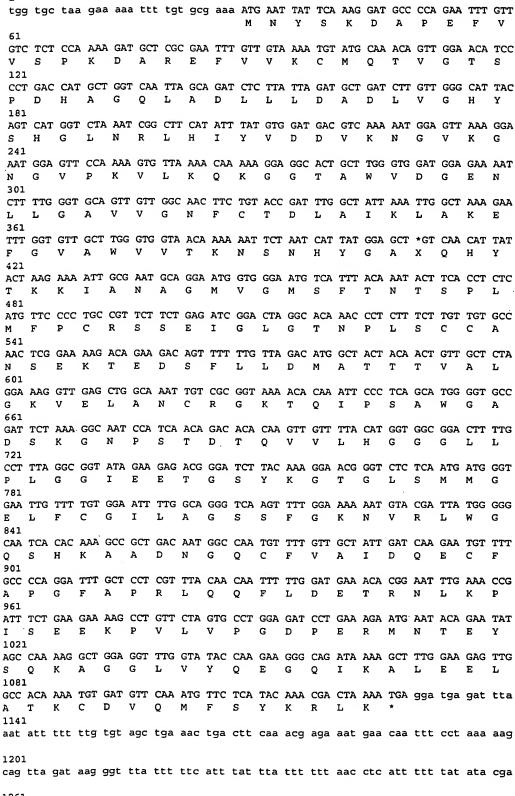
acg aga aat gaa caa ttt cct aaa aag cag tta gat aag ggt tta ttt ttc att tta

ttt ttt aac ctc att ttt tat ata cga ata aaa tta atg ctc \*aa aaa aaa aaa aaa aaa

FIG. 1



Appln No.: 60.848 Applicant(s): Andrew Kloek et al. NEMATODE MDH-LIKE SEQUENCES





age aga tat gac tga aac tgg agg tgg tga ttc tgt tga atc tgc aag tgt tta tgc taa

FIG. 2B

## Applications): Andrew Kloek et al. NEMATODE MDH-LIKE SEQUENCES

ctc tgt ttg tga aat gtg cgg aaa tta tga ggt tca act tca aac aat tca aag cag tca

1381
gga tac tct cag gga gaa att ggc agc tgc taa aga att gta tga gaa ata tgg caa gga

1441
att gac aga aga gag gca tta tcg aaa gga att gga aat taa att tgc tgc ttt aaa tga

1501
aga aac tga agg gaa aat tca gca atg tat tac caa tac aga aga ctt tga cag cgt att

1561
gcc ttc tca gta aaa aac aa\* aag ctg att tgt ctg ttt tgg aat c\*c aat tag aat tgg

1621
cta gga atc gtc aaa aag agc ttc aag aac aat tgg ttt tgt taa atg aaa ggt atg aaa

1681
aac ttt tac att taa aat ctc aat gtg ctg aag aaa tgc gtg aac aac aaa ttg ac tgc

1721
ctc aaa cag ttg aag aac ttc aat ttt tgg cat tgc agt tga \*ag agg aat tga taa ctg

1781
aac gtg cag cac gtg agc atg aaa gga ggg aat taa atg atg aat tgg cta tgg cac gtc

1841
aac agc ttg ttg aat tgg aaa ttt gtc c\*a gag aaa atg aag aat gaa ttt tat gat ata

1901
taa aaa tat att tat ttt gct caa ata g\*t ttt ata aat ttt aag agc tga tag aaa aat

tta gtt ttg \*aa ttt ttg aag aat ata ttt t\*t acg gtt tgc ac\* cct tag aat ggt ttt

gtt tta ata aat gc\* c\*g gtt gg\* aaa aaa aaa aaa aaa aaa aaa

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2021



## Amino acid alignment

*M. incognita* MDH1 *M. incognita* MDH2 *C. elegans* MDH1 *C. elegans* MDH2

1 2 3 4	
1 2 3 4	
1 2 3 4	130 140 150 160 170 180  GTAWVDGEFILIGAVVGNFCTDLAIKLAKEFGVAWVVTKNSNHYGACQHYTKKIANAGMVG:142 GTAWVDGEFILIGAVVGNFCTDLAIKLAKEFGVAWVVTKNSNHYGACQHYTKKIANAGMVG:142 STAWVDGNFLLGPVVGNFCMQLAVEKAKEFGIGWVVCRNSNHFGIAGWYADFACRNGLVG:148 GTAWVDGNFLLGPVVGNFCMDLAIEKAKNAGIGWVVAKGSNHYGIAGWYALRAMKKGMLG:180
1 2 3 4	190 200 210 220 230 240  MSETHTSPLMFPCRSSEIGLGTHPLSCCVHSEKTGDSFLIDMATHTVALGKVELADCRGK:202  MSETHTSPLMFPCRSSEIGLGTHPLSCCANSEKTEDSFLIDMATHTVALGKVELAHCRGK:202  MAFTHTSPCVFPTGSREKSLGSHPI.CMAAPGMEGDSFFLIDMASHTVAVGKIEVVDRKGE:207  MSMTHTSPISFTRSAVPALGTHPI.SLAAPGTGDDSFVLDMASHTVAIGKVELAARK.E:238
1 2 3 4	250 260 270 280 290 300  TQIPSTWGADSKGUPSTDTQVVLHGGGLLPLGGIEETGSYKGTGLSMMGELFCGILAGSS:262  TQIPSAWGADSKGUPSTDTQVVLHGGGLLPLGGIEETGSYKGTGLSMMGELFCGILAGSS:262  TYIPGSWGADKUGDETHUPKEVLDGGGLQPLGGSEITGGYKGTGLCMMVEVLCGIMGGSA:267  NPVPLSWGVGEGGKETTDPTKVLYGGGLLPLGGVEVSGGYKGYGLSSMIEIFCGILAGAH:298
2	310 320 330 340 350 360  EGKIVELWGQSHKAADUGQCEVAIDQECFAPGFAPRLQQELDETRILKPISEEKPVLVPG:322  EGKIVELWGQSHKAADUGQCFVAIDQECFAPGFAPRLQQELDETRILKPISEEKPVLVPG:322  EGKIIRQWQTTSKTADLGQCFVAIDPECFAPGFSBRLQEFCDETRILUPINPSRPPQVPG:327  WGPHVRKWMSTKSEADLGQCFVAIDPEAFAPGFADRLQDBMQTMRALPTSSPSFKVEVAG:358
1 2 3 4	DPERMUTEYSQKAGGLVYQEGQIKALEELATKCDVQMFSYKRLK.:366 DPERMUTEYSQKAGGLVYQEGQIKALEELATKCDVQMFSYKRLK.:366 DPERMUTEYSQKAGGLVYQEGQIKALEELATKCDVQMFSYKRLK.:366 DPERAHMUMCDDLGGIVYKKKQLDHUKULADRLGVILMRLVDEKPQ:372 DMERRHEALVEQLGGIPYHKUQITFVNDLAAKLGVKTVDLVQ:400